

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:	Debatin <i>et al.</i>	Filed via EFS Web April 1, 2008
Title:	SMAC-PEPTIDES AS THERAPEUTICS AGAINST CANCER AND AUTOIMMUNE DISEASES	
Appl. No.:	10/511,037	
§371 Date:	January 19, 2005	
I.A. Filing Date	April 17, 2003	
Examiner:	Hong Sang	
Art Unit:	1643	
Confirmation Number:	6277	

**STATEMENT AND DECLARATION TO SUPPORT FILING AND SUBMISSION OF
SEQUENCE LISTING BY AMENDMENT IN ACCORDANCE WITH
37 C.F.R. § 1.57(f)**

Commissioner for Patents
P.O. Box 1450
Alexandria, Virginia 22313-1450

Sir:

In connection with a Sequence Listing submitted concurrently herewith for insertion into the captioned specification, the undersigned hereby declares that the material being inserted by amendment is the material previously incorporated by reference and that the amendment contains no new matter.

The sequence listing submitted herewith includes the sequences from GenBank accession numbers disclosed in the captioned application and priority documents EP 02008199.8 and EP 02015499.3. Specifically, the sequence listing includes the Smac polypeptide of GenBank accession no. AAF87716 (SEQ ID NO:1), the polynucleotide encoding the Smac polypeptide as disclosed in GenBank accession no. AF262240 (SEQ ID NO:2), the HIV-1 tat polypeptide of GenBank accession no. CAA45921 (SEQ ID NO:3) and the polynucleotide encoding the HIV-1 Genome of GeneBank accession no. M15654 (SEQ ID NO:4).

The GenBank accession numbers referred to above may be found on page 4, line 15; page 6, lines 9-10; and page 16, line 1 of the International Publication No. WO 03/086470, which corresponds to the present application. Additionally, the GenBank accession numbers AAF87716, AF262240; and CAA45921 may be found in priority document EP 02015499.3 on page 2, line 28; page 6, lines 4-5 and page 12, lines 15-16. Finally, the GenBank accession numbers AAF87716, AF262240; and M15654 may be found in priority document EP 02008199.8 on page 2, line 28; page 6, line 5 and page 15, line 4.

Submitted herewith as Exhibits 1-4 are copies of each of the GenBank entries and their respective sequence revision histories. Genbank accession numbers AAF87716 and AF262240 have never been revised since their original GenBank submission. *See* Exhibits 1-2. GenBank accession numbers CAA45921 and M15654 have been revised, however the version numbers of the sequences have remained the same as indicated on the sequence revision history of each submission. *See* Exhibits 3 and 4. The revisions indicated in the histories for GenBank accession numbers CAA45921 and M15654 do not relate to sequence revisions. A revision of a sequence itself would have changed the version number of the sequence, according to the National Center for Biotechnology Information (NCBI). As such, the undersigned believes that the amendment to add the sequence listing filed herewith does not introduce new matter.

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,

Date April 1, 2008

FOLEY & LARDNER LLP
Customer Number: 22428
Telephone: (202) 672-5404
Facsimile: (202) 672-5399




By

for

Michele M. Simkin
Attorney for Applicant
Registration No. 34,717

Reg # 54,161

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Range: from to
 Features: ☒ CDD

☐ 1: [AAF87716](#). Reports Smac [Homo sapien...[gi:9454219]

[BLink](#), [Conserved Domains](#), [Links](#)

Features Sequence

LOCUS AAF87716 239 aa linear PRI 26-JUL-2000
 DEFINITION Smac [Homo sapiens].
 ACCESSION AAF87716
 VERSION AAF87716.1 GI:9454219
 DBSOURCE locus AF262240 accession [AF262240.1](#)
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 239)
 AUTHORS Du,C., Fang,M., Li,Y., Li,L. and Wang,X.
 TITLE Smac, a mitochondrial protein that promotes cytochrome c-dependent
 caspase activation by eliminating IAP inhibition
 JOURNAL Cell 102 (1), 33-42 (2000)
 PUBMED 10929711
 REFERENCE 2 (residues 1 to 239)
 AUTHORS Du,C., Fang,M., Li,Y. and Wang,X.
 TITLE Direct Submission
 JOURNAL Submitted (01-MAY-2000) Howard Hughes Medical Institute and
 Department of Biochemistry, University of Texas Southwestern Medical
 Center, 5323 Harry Hines Blvd., Dallas, TX 75235, USA
 COMMENT Method: conceptual translation supplied by author.
 FEATURES Location/Qualifiers
 source 1..239
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 Protein 1..239
 /product="Smac"
 /function="binds IAPs and neutralizes their inhibition on
 caspase activation and activity"
 /name="antagonist of IAPs (inhibitors of apoptosis)"
 transit peptide 1..55
 /note="mitochondrial targeting sequence"
 Region 6..239
 /region_name="Smac_DIABLO"
 /note="Second Mitochondria-derived Activator of Caspases;
 pfam09057"
 /db_xref="CDD:72475"
 CDS 1..239
 /coded_by="AF262240.1:20..739"

ORIGIN

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181 itarnhiqlv klqveevhql srkaetklae aqieelrqkt qeegeeraes egeaylred
```

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Sequence Revision History

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Revision history for AAF87716

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GI	Version	Update Date	Status
9454219	1	Jul 26 2000 12:05 AM	Live

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multiple taxa

Accession AAF87716 was first seen at NCBI on Jul 26 2000 12:05 AM

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Send to

Hide: ☐ sequence☐ all but gene, CDS and mRNA

Range: from begin

to end

☐ Reverse complemented strandFeatures: ☐ SNP

+

Refr

☐ 1: AF262240. Reports Homo sapiens Smac...[gi:9454218]

Links

Features Sequence

LOCUS AF262240 1358 bp mRNA linear PRI 26-JUL-2000

DEFINITION Homo sapiens Smac mRNA, complete cds; nuclear gene for mitochondrial product.

ACCESSION AF262240

VERSION AF262240.1 GI:9454218

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1358)

AUTHORS Du,C., Fang,M., Li,Y., Li,L. and Wang,X.

TITLE Smac, a mitochondrial protein that promotes cytochrome c-dependent caspase activation by eliminating IAP inhibition

JOURNAL Cell 102 (1), 33-42 (2000)

PUBMED 10929711

REFERENCE 2 (bases 1 to 1358)

AUTHORS Du,C., Fang,M., Li,Y. and Wang,X.

TITLE Direct Submission

JOURNAL Submitted (01-MAY-2000) Howard Hughes Medical Institute and Department of Biochemistry, University of Texas Southwestern Medical Center, 5323 Harry Hines Blvd., Dallas, TX 75235, USA

FEATURES

source Location/Qualifiers

1..1358

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

CDS 20..739

/function="binds IAPs and neutralizes their inhibition on caspase activation and activity"

/note="antagonist of IAPs (inhibitors of apoptosis)"

/codon_start=1

/product="Smac"

/protein_id="AAF87716.1"

/db_xref="GI:9454219"

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transit_peptide 20..184

/note="mitochondrial targeting sequence"

ORIGIN

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661 agagctccgt  cagaaaacac  aggaggaagg  ggaggagcgg  gctgagtcgg  agcaggaggc
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1261 gagtgaaaaa  cctattacta  ctaagagaag  ggggtgcagag  tgtttacctg  gtgctctcaa
1321 caggacttaa  catcaacagg  acttaacaca  gaaaaaaaa
```

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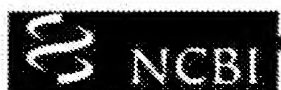


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GI	Version	Update Date	Status
9454218	1	Jul 26 2000 12:05 AM	Live

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 Features: ☒ CDD

☐ 1: CAA45921. Reports HIV-1 tat [Human ...[gi:60145]

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LOCUS CAA45921 86 aa linear VRL 20-NOV-1992
 DEFINITION HIV-1 tat [Human immunodeficiency virus 1].
 ACCESSION CAA45921
 VERSION CAA45921.1 GI:60145
 DBSOURCE embl accession [X64650.1](#)
 KEYWORDS .
 SOURCE Human immunodeficiency virus 1 (HIV-1)
 ORGANISM Human immunodeficiency virus 1
 Viruses; Retro-transcribing viruses; Retroviridae;
 Orthoretrovirinae; Lentivirus; Primate lentivirus group.
 REFERENCE 1 (residues 1 to 86)
 AUTHORS Siderovski,D.P., Matsuyama,T., Frigerio,E., Chui,S., Min,X.,
 Erfle,H., Sumner-Smith,M., Barnett,R.W. and Mak,T.W.
 TITLE Random mutagenesis of the human immunodeficiency virus type-1
 trans-activator of transcription (HIV-1 Tat)
 JOURNAL Nucleic Acids Res. 20 (20), 5311-5320 (1992)
 PUBMED [1437550](#)
 REFERENCE 2 (residues 1 to 86)
 AUTHORS Siderovski,D.P.
 TITLE Direct Submission
 JOURNAL Submitted (26-FEB-1992) D.P. Siderovski, Dept of Medical
 Biophysics, University of Toronto, 500 Sherbourne Street, Toronto
 Ontario M4X 1K9, CANADA
 FEATURES Location/Qualifiers
 source 1..86
 /organism="Human immunodeficiency virus 1"
 /db_xref="taxon:11676"
 Protein 1..86
 /product="HIV-1 tat"
 Region 2..>47
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 /note="Transactivating regulatory protein (Tat). The
 retroviral Tat protein binds to the Tar RNA. This
 activates transcriptional initiation and elongation from
 the LTR promoter. Binding is mediated by an arginine rich
 region; pfam00539"
 /db_xref="CDD:84847"
 CDS 1..86
 /gene="HIV-1 tat"
 /coded_by="X64650.1:39..299"
 /db_xref="InterPro:IPR001831"
 ORIGIN

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1 mepvdprlep wkhpgsqpkt actncycckc cfhcqvcfit kalgisygrk krrqrrrppq
61 gsqthqvsls kqptsqsrqd ptgpke
```

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GI	Version	Update Date	Status	I	II
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60145	1	Aug 8 2003 11:42 PM	Dead	<input type="radio"/>	<input checked="" type="radio"/>
60145	1	Oct 19 2002 2:32 PM	Dead	<input type="radio"/>	<input type="radio"/>
60145	1	Mar 8 1999 10:26 PM	Dead	<input type="radio"/>	<input type="radio"/>
60145	1	May 25 1995 12:46 PM	Dead	<input type="radio"/>	<input type="radio"/>
60145	1	Dec 1 1994 11:51 AM	Dead	<input type="radio"/>	<input type="radio"/>
60145	1	Sep 1 1993 8:12 PM	Dead	<input type="radio"/>	<input type="radio"/>
60145	1	Apr 21 1993 5:17 PM	Dead	<input type="radio"/>	<input type="radio"/>

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Range: from begin

to end

☐ Reverse complemented strand

Features: +

Refresh

☐ 1: M15654. Reports Human immunodeficiency virus type 1, isolate BH10, genome.

Links

Comment Features Sequence

LOCUS HIVBH102 8932 bp ss-RNA linear VRL 02-AUG-2006

DEFINITION Human immunodeficiency virus type 1, isolate BH10, genome.

ACCESSION M15654 K02008 K02009 K02010

VERSION M15654.1 GI:326383

KEYWORDS TAR region; acquired immune deficiency syndrome; env protein; gag protein; long terminal repeat (LTR); pol protein; polyprotein; proviral gene; reverse transcriptase; transactivator.

SEGMENT 2 of 2

SOURCE Human immunodeficiency virus 1 (HIV-1)

ORGANISM Human immunodeficiency virus_1

Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae; Lentivirus; Primate lentivirus group.

REFERENCE 1 (bases 1 to 8932)

AUTHORS Wong-Staal,F., Gallo,R.C., Chang,N.T., Ghrayeb,J., Papas,T.S., Lautenberger,J.A., Pearson,M.L., Petteway,S.R.Jr., Ivanoff,L., Baumeister,K., Whitehorn,E.A., Rafalski,J.A., Doran,E.R., Josephs,S.J., Starcich,B., Livak,K.J., Patarca,R., Haseltine,W.A. and Ratner,L.

TITLE Complete nucleotide sequence of the AIDS virus, HTLV-III

JOURNAL Nature 313 (6000), 277-284 (1985)

PUBMED 2578615

REFERENCE 2 (bases 1 to 8932)

AUTHORS van Beveren,C.P., Coffin,J. and Hughes,S.

TITLE Appendix B: HTLV-3 genome

JOURNAL (in) Weiss,R.L., Teich,N., Varmus,H. and Coffin,J. (Eds.); RNA TUMOR VIRUSES, MOLECULAR BIOLOGY OF TUMOR VIRUSES, SECOND EDITION, 2; Cold Spring Harbor Laboratory, CSH, NY (1985)

REFERENCE 3 (sites)

AUTHORS Hostomsky,Z., Hostomska,Z., Hudson,G.O., Moomaw,E.W. and Nides,B.R.

TITLE Reconstitution in vitro of RNase H activity by using purified N-terminal and C-terminal domains of human immunodeficiency virus type 1 reverse transcriptase

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1148-1152 (1991)

PUBMED 1705027

COMMENT Original source text: Human immunodeficiency virus type 1 (HIV-1) proviral DNA clone BH10.

[(in) Weiss,R., Teich,N., Varmus,H. and Coffin,J. (Eds.);RNA Tumor Viruses,Molecu] review; bases 1 to 8932.

The BH10 sequence differs from BH8 and BH5 by 0.9% in the coding regions and 1.8% in the noncoding regions, and the authors of [1] believe that these are stable variants.

The HTLV-III genome encodes at least seven proteins: gag, pol, env,

tat, trs, 27K antigen and the sor 23K product. The 3' ORF (positions 8153-8773) is truncated in BH10 (stop codon at positions 8522-8524), but reads through in BH8 and other sequences to yield what is now called the 27K antigen.

The mechanism for pol gene translation has not been elucidated: a gag-pol fusion protein is possible; splicing or frameshift have not been ruled out. The viral protease would be determined by the region in question.

The Tat protein (trans-activator protein, approximately 14 kb) is an effector of an autostimulatory pathway through interaction with a positive control element, the trans-activating responsive sequence, TAR. Tat seems to be a transcriptional control molecule in HTLV-I, but is both that and a post-transcriptional regulatory molecule in HTLV-III. Deletion mutants in the tat gene are incapable of prolific replication and exhibit no cytopathic effects in T4+ cell lines.

In addition to the

9.4 kb genomic mRNA, subgenomic mRNAs of 7.4, 5.5, 5.0, 4.3, 2.0 and 1.8 kb have been detected.

FEATURES	Location/Qualifiers
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prim transcript	<1..>8932 /note="tat, rev, nef subgenomic mRNA"
intron	66..5135 /note="tat, rev, nef subgenomic mRNA intron 1"
gene	112..1650 /gene="gag"
CDS	112..1650 /gene="gag" /codon_start=1 /product="gag polyprotein precursor" /protein_id="AAA44201.1" /db_xref="GI:326388" /translation="MGARASVLSGGELDRWEKIRLRPGGKKKYKCLKHIVWASRELERF AVNPGLLLETSEGCROILGQLQPSLQTGSEELRSLYNTVATLYCVHQRIEIKDTKEALD KIEEEQNKSKKKAQQAADTGHSSQVSQNYPIVQNIQGMVHQAI SPRTLNAWVKVVE EKAFSPEVIPMFSA LSEGATPQDLNTMLNTVGGHQAAMQMLKETINEEAAEWDRVHPV HAGPIAPGQMREPRGSDIAGTTSTLQEQIGWMTNNPPIPVGEIYKRWIILGLNKIVRM YSPTSILDIRQGPKPEFRDYVDRFYKTLRAEQASQEVKNWMTETLLVQNANPDCKTIL KALGPAATLEEMMTACQGVGGPGHKARVLAEAMSQVTNTATIMMQRGNFRNQRKMVKC FNCGKEGHTARNCRAPRKKGCWKCGKEGHQMKDCTERQANFLGKIWP SYKGRPGNFLQ SRPEPTAPPFLQSRPEPTAPPEESFRSGVETTTTPQKQEPIDKELYPLTSLRSLFGND PSSQ"
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CDS	<1407..4454 /gene="pol" /note="ORF for pol polyprotein containing stop codons" /codon_start=1 /product="pol polyprotein" /protein_id="AAA44198.1" /db_xref="GI:326385" /translation="FFREDLAF LQ GKAREFSSEQTRANSPTISSEQTRANSPTRELO VWGRDNNSPSEAGADRQGTVSFNFPQITLWQRPLVTIKIGGQLKEALLDTGADDTVLE EMSLPGRWKPKMIGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTP VNIIGRNLLTQ"

```

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VTNKGROKVVPLTNTTNQKTELQAIYLALQDSGLEVNIVTDSQYALGIIQAQPKSES
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VILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKTIHTDNGSNFTSATVKAA
CWWAGIKQEFGIPYNPQSQGVVESMNKELKKIIGQVRDQAEHLKTAVQMAVFIHNFKR
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